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**Suspect Screening of Large Numbers of Emerging Contaminants in
Environmental Waters using Artificial Neural Networks for Chromatographic
Retention Time Prediction and High Resolution Mass Spectrometry Data Analysis**

Richard Bade¹, Lubertus Bijlsma¹, Leon Barron², Thomas Miller², Juan Vicente Sancho¹, Felix Hernández^{1*}

¹*Research Institute for Pesticides and Water, University Jaume I, Avda. Sos Baynat, E-12071 Castellón, Spain.*

²*Analytical & Environmental Sciences Division, Faculty of Life Sciences and Medicine, King's College London, 150 Stamford Street, London SE1 9NH, United Kingdom*

*Corresponding author: felix.hernandez@uji.es Tel.: +34 964 387366 Fax: +34 964 387368

Abstract:

The recent development of broad-scope high resolution mass spectrometry (HRMS) screening methods has resulted in a much improved capability for new compound identification in environmental samples. However, positive identifications at the ng/L concentration level rely on analytical reference standards for chromatographic retention time (t_R) and mass spectral comparisons. Chromatographic t_R prediction can play a role in increasing confidence in suspect screening efforts for new compounds in the environment, especially when standards are not available, but reliable methods are lacking. The current work focuses on the development of artificial neural networks (ANNs) for t_R prediction in gradient reversed-phase liquid chromatography and applied along with HRMS data to suspect screening of wastewater and environmental surface water samples. Based on a compound t_R dataset of >500 compounds, an optimized 4-layer back-propagation multi-layer perceptron model enabled predictions for 85 % of all compounds to within 2 minutes of their measured t_R for training (n=344) and verification (n=100) datasets. To evaluate the ANN ability for generalization to new data, the model was further tested using 100 randomly selected compounds and revealed 95 % prediction accuracy within the 2-minute elution interval. Given the increasing concern on the presence of drug metabolites and other transformation products (TPs) in the aquatic environment, the model was applied along with HRMS data for preliminary identification of pharmaceutically-related compounds in real samples. Examples of compounds where reference standards were subsequently acquired and later confirmed are also presented. To our knowledge, this work presents for the first time, the successful application of an accurate retention time predictor and HRMS data-mining using the largest number of compounds to preliminarily identify new or emerging contaminants in wastewater and surface waters.

Keywords: Retention time prediction, artificial neural networks, time-of-flight high resolution mass spectrometry, screening of emerging contaminants

1. Introduction

The number of emerging contaminants in the aquatic environment is increasing, due to urbanization and subsequent societal and industrial needs (Pal et al., 2014). The development of liquid chromatography-high resolution mass spectrometry (LC-HRMS) technologies has revolutionized the analysis of emerging contaminants in environmental waters, and especially for screening of large numbers of compounds (Agüera et al., 2013; Gómez et al., 2010; Hernández et al., 2011; Hogenboom et al., 2009). HRMS instruments allow the recording of full-scan spectra with high mass accuracy and resolution, thus making it possible to search for any given compound based on its exact mass.

There has been much interest in improving the confidence in the identification of small molecules with HRMS; from potential positives through to detection and finally confirmation (Hernández et al., 2015a; Schymanski et al., 2014). The main distinguishing factor between these levels is the (non-) availability of reference standards. Suspect screening refers to compounds tentatively identified based solely on HRMS data and comparable spectral libraries. Confirmation requires reference standards. An additional tool to increase the confidence in the tentative identification of compounds for which standards are unavailable is reliable and accurate t_R prediction. This is of particular relevance in the case of degradation/transformation products (TPs), which can reach the aquatic environment in high concentrations, but commonly for which reference standards are less accessible. Chemical risk assessment is therefore significantly challenging for such compounds.

Prediction of t_R plays an important role in the qualitative identification of emerging contaminants. Many different approaches to t_R prediction exist and range from the simple (Kern et al., 2009; Nurmi et al., 2012) to the complex (Goryński et al., 2013; Ji et al., 2009; Kaliszan et al., 2003; Ukić et al., 2014a). For example, $\log K_{ow}$ models can be derived using freely accessible data from chemical databases such as ChemSpider and PubChem, as well as freeware prediction sources such as VCCLABS. Its use in t_R prediction is extremely simple to implement. It is frequently used in environmental studies for the description of the fate of various pollutants and as a simple t_R predictor for TPs (Kern et al., 2009) and emerging contaminants (Bade et al., 2015; Nurmi et al., 2012). Alongside simple algorithms, other and more complex *in*

silico approaches now exist which are based on quantitative structure-retention relationship (QSRR) modeling, including artificial neural networks, support vector machines and random forests (Giaginis and Tsantili-Kakoulidou, 2012; Héberger, 2007). The principal aim of QSRR is to predict retention data from the molecular structure and its physicochemical properties, using a range of input descriptors and measured t_R data. One QSRR method gaining recent attention for broad screening using high resolution techniques is the use of artificial neural networks (ANNs), a predictive computing technique that has shown itself as a promising t_R predictor with potentially higher accuracy than classical models (Miller et al., 2013; Ukić et al., 2014b). The design of ANNs were inspired by the human brain and differ from classical computer programs in that they generally employ non-linear learning techniques using a set of case examples (i.e. a training dataset) (Kaliszan et al., 2003). In the training phase, the ANN requires a range of suitable molecular descriptors as well as the true output value (in this case, measured t_R) to use for comparison with predicted values. At the same time, a second dataset of case examples is often used for verification and to assess overall ANN predictive error. The true output values in the verification set are generally not employed for learning, but the number of training cycles can be stopped by the user or the software when the overall measured error across all cases is at its minimum. Therefore, ANN learning is generally an iterative process and once an acceptable number of training cycles is reached, the optimized ANN can be applied to predict the output where experimentally derived data are unavailable (Miller et al., 2013). In some cases, a third dataset can be used after the model has been finalized to ‘blind test’ the predictive power of the network. Its use is even more pertinent for analyses where large number of new analytes are expected to occur and with potentially high variance from sample to sample, such as in environmental and municipal water samples. Therefore, since information from the sample includes chromatographic t_R as well as HRMS data, it makes this interpretation of suspect occurrence more accessible in the first instance.

The aim of this work was to develop and evaluate ANN for predictions of unknown chromatographic t_R in suspect screening of environmental waters. To the best of our knowledge, this method includes the largest range of physicochemically diverse compounds for this purpose (n=544 in total) and includes both neutral and charged compounds eluted under gradient reversed-phase LC conditions. Lastly, this work aimed to improve upon a recent $\log K_{ow}$ -based t_R prediction approach (Bade et al., 2015)

using the ANNs as an alternative. This work, for the first time, presents the use of ANN for identification of additional suspect compounds (including metabolites and TPs) in wastewater and surface water samples both with and without reference standards.

2. Experimental

2.1 Reagents and Chemicals

A total of 544 analytical grade reference materials were used for preparation of model solutions at 25 µg/L or 50µg/L (diluted from mixed standard solutions in methanol or acetonitrile with water) for ANN modeling of t_R . These included pesticides, drugs of abuse, human/veterinary pharmaceuticals and mycotoxins (See Supplementary Information (SI) Table S1 for all compounds used in this study). These covered a large range of molecular hydrophobicity ($\log K_{ow}$ -3 to 9). Information relating to 595 standards was available (Bade et al., 2015), however after transforming the compounds using SMILES codes, some errors were observed, leading to incomplete data, and a further 42 were removed from the initial ANN method development (Section 3.1) to use in a subsequent blind test (Section 3.2). Further details relating to these compounds can be found elsewhere (Bade et al., 2015; Hernández et al., 2015b).

2.2 Water samples for suspect identification

A total of 44 composite (24-h) influent and effluent wastewater (IWW and EWW) samples and grab surface water (SW) samples were used to demonstrate the application of the developed ANN model. All these samples were previously used in different studies performed at our lab using the same analytical instrumentation for analysis. (Hernández et al., 2015a) All measured t_R data herein were generated using ultra-high pressure liquid chromatography coupled to quadrupole-time of flight mass spectrometry (UHPLC-QTOF-MS).

2.3 UHPLC-QTOF MS

A Waters Acquity UPLC system (Waters, Milford, MA, USA) was interfaced to a hybrid quadrupole-orthogonal acceleration-TOF mass spectrometer (XEVO G2 QTOF, Waters Micromass, Manchester, UK), using a electrospray ionization (ESI) Z-Spray interface operating in positive mode. The chromatographic separation was performed using an Acquity UPLC BEH C₁₈ 100 × 2.1 mm, 1.7µm particle size column (Waters) at

a flow rate of 300 $\mu\text{l}/\text{min}$. Gradient elution was performed using mobile phases of A= H_2O and B= MeOH , both containing 0.01% HCOOH . The initial percentage of B was 10%, which was linearly increased to 90% in 14 min, followed by a 2 min isocratic period and, then, returned to initial conditions during 2 min. The total run time was 18 min. Nitrogen was used as the drying gas and nebulizing gas.

MS data were acquired over an m/z range of 50–1000. A capillary voltage of 0.7 kV and cone voltage of 20 V were used. Collision gas was argon 99.995 % (Praxair, Valencia, Spain). The desolvation temperature was set to 600°C , and the source temperature to 135°C . The column temperature was set to 40°C . MS data was acquired in MS^E mode, selecting a collision energy of 4 eV for low energy (LE) and a ramp of 15–40 eV for high energy (HE). The LE and HE functions settings were for both a scan time of 0.4s. (Hernández et al., 2011; Ibáñez et al., 2013)

Processing of MS data was made using ChromaLynx XS application manager (within MassLynx v 4.1; Waters Corporation). The following parameters were used: mass window 0.020 Da (for positive ID ≤ 0.010 Da), peak width at 5% height: 6 seconds, peak-to-peak baseline noise: 1000 and threshold absolute area 500. When manually searching the data for all peaks in an eXtracted Ion Chromatogram (XIC), a chromatographic peak was thought viable when above an intensity threshold of 3000 counts.

2.4 Molecular description and neural network optimization procedures

The molecular descriptors chosen were based on the previous work of Miller *et al*, wherein more than 200 descriptors were evaluated. (Miller et al., 2013) As the same type of column and LC system were used in both studies, the same descriptors were hoped to provide similar results. Compound $\log D$ data (for a mobile phase of $\text{pH}=3.2$) were generated using Percepta PhysChem Profiler (ACD Laboratories, ON, Canada) and for all other descriptors, Parameter Client freeware was used (Virtual Computational Chemistry Laboratory, Munich, Germany). Canonical simplified molecular line entry system strings (SMILES) were created using ChemSpider freeware (Royal Society of Chemistry, UK) for 544 compounds and from these 16 molecular descriptors (as ANN inputs) were generated including the number of double and triple bonds (nDB or nTB), the number of carbon and oxygen atoms (nC or nO), the number of 4–9 membered rings (nR04–nR09), unsaturation index (UI), hydrophilic factor (Hy),

Moriguchi and Ghose-Crippen logP (MlogP and AlogP respectively) as well as with software predicted log K_{ow} data (Tetko et al., 2005). Prediction of t_R (as the designated single output) via neural networks was performed using Trajan version 6.0 neural network simulator (Trajan Software Ltd., Lincolnshire, U.K.) and compared with experimentally determined t_R via correlation graphs as well as assessment of residual errors. Table S1 has all compounds and their respective predicted and experimental t_R and ANN subset.

3. Results and Discussion

In a previous study, we developed a simple t_R prediction model based on log K_{ow} of nearly 600 compounds, predicted using freeware (Bade et al., 2015). This resulted in approximately 70 % of all compounds being predicted within 2 minutes of the measured t_R , and 95 % within 4 minutes. This technique was simple to implement and facilitated the removal of several false positives. However, when investigating unknowns and compounds for which reference standards were unavailable, it was concluded that a more robust, accurate and precise methodology was still needed. In this vein, ANNs were considered as an alternative. Recent work successfully used ANN for a similar purpose, albeit using a much smaller set of compounds of 86 and 166 compounds in either study and focused only on pharmaceuticals (Miller et al., 2013; Munro et al., 2015). It is unlikely that this fully represents the breadth of alternative compound classes and chemistries potentially occurring simultaneously in environmental waters. However, these models successfully predicted t_R for a range of blind test drug compounds in wastewater and urine to warrant further investigation here using a much larger case dataset.

3.1 Prediction of t_R using Artificial Neural Networks (ANNs)

Over 100,000 network architectures for each model type were initially investigated for their predictive ability across five different ANN model types including 3- and 4-layer multi-layer perceptrons (MLPs), generalized regression neural networks (GRNNs), radial basis functions (RBFs), linear neural networks and probabilistic neural networks

(PNN). For training, 344 cases were used along with 100 cases for both verification and blind testing of network performance. Cases were randomly assigned at the beginning of each network test. The diversity of ANN types and architectures tested was balanced against the error generated. For network design and testing the omission of input descriptors was included as an option. One hundred of the best networks (software selected) were retained for further investigation which mainly comprised of MLPs, GRNNs and RBFs. Overall for this separation system, the best correlations of predicted versus experimentally measured t_R were observed using MLPs in comparison to all other types and these correlations were in agreement with previous works despite different compounds being used for training, verification and blind testing (Barron et al., 2009; Miller et al., 2013; Munro et al., 2015). The finalized network was found to be a 4-layer 16-19-9-1 MLP using all 16 molecular descriptors as inputs (**Figure 1**). This ANN type and architecture was chosen based on the lowest absolute errors (i.e. predicted t_R -measured t_R) in the training, verification and blind test sets across all networks. As seen, the correlation coefficients (R^2) are between 0.86 and 0.90 between the three sets, already a marked improvement on that from our previous study of 0.67 (Bade et al., 2015).

The maximum measured t_R on this chromatographic system was 16.50 min (narsin; an antibiotic) and the lowest was 0.86 min (methamidophos; an organophosphate insecticide). For all compounds within this retention window of 15.64 min, the mean error in t_R prediction was <6 % using this ANN approach for all compounds. Overall, the mean absolute errors and standard deviations were recorded as 0.97 ± 0.95 min (training set); 0.79 ± 0.85 min (verification set); 0.79 ± 0.69 min (blind test set); and 0.91 ± 0.89 min (all sets combined). When focussing specifically on the blind test set which was used to simulate a true application of the approach, 95 % of compounds had predicted t_R values within 2.00 min of the measured value and the maximum error was 3.56 min for metosulam (**Figure 2**). However, across the other datasets some larger errors were recorded in isolated cases. **Table 1** shows that for all datasets, 90% of all 544 compounds could be predicted to within 2.00 min of the measured t_r value. Upon sub-division of the datasets, 85 % of the compounds in the training and verification sets and 95% of compounds in the blind test set were predicted to within two minutes of the measured value. The maximum error recorded within the training set was +6.25 min (for the beta blocker atenolol; measured t_r =2.49 min); within

the verification set was +5.19 min (for the anti-helminthic drug levamisole; measured t_R =3.02 min) and within the blind test set was +3.56 min (for the pesticide, metosulam; measured t_R =7.54 min).

Prediction errors for all cases were investigated again with respect to any apparent trends and it was found that a very slight over-estimation existed for poorly retained compounds, as well as the converse for strongly retained compounds. Recent work focussing on modelling a smaller number of compounds in wastewater also revealed a similarly slight bias, but used a different network type (a GRNN)(Munro et al., 2015). When examining those compounds with absolute errors >2.00 min (54 compounds in total across all sets), these were spread across the entire compound retention range (mean measured t_R =7.81±3.93). However, a slight over-estimation was again apparent for 29 compounds with t_R from 1.34-5.38 min (mean measured t_R = 2.97 min). Reduced under-estimation was observed for the remaining 25 compounds eluting between 5.38-16.30 min (mean measured t_R = 10.67 min for these compounds). Seventeen compounds eluting <5.38 min were over-estimated and t_R for eleven were under-estimated when eluting >10.00 min.

The contribution of each descriptor towards the final prediction output was investigated using the ANN software sensitivity analysis tool. In this test, each molecular descriptor is removed and treated as missing by the ANN. A new predicted t_R is generated and a ratio calculated between the network error with a given input omitted to the error of the network with a complete input dataset. Ratios >1 indicated higher importance in the prediction. Perhaps not surprisingly for a reversed-phase chromatography system, the most important molecular descriptors and their measured error ratios were: logD (1.443), log K_{ow} (1.182), AlogP (1.114), nO (1.096), UI (1.006) MlogP (1.023), Hy (1.017), nDB (1.012), nR04-nR09 (all 1.000-1.063), nTB (1.004) and nC (1.002). The lowest ratio was observed for nR04 with a ratio of 1.000 meaning no change in network performance was measured for its removal. However within the dataset, only 14 compounds had 4-membered rings (amoxicillin, ampicillin, cefaclor, cefadroxil, cefalexin, cefotaxime, cefquinome, cefuroxime, cloxacillin, dicloxacillin, heptenophos, oxacillin, oxasulfuron, and penicillin G). Inclusion of nR04 still resulted in better performance in comparison to any other type or architecture investigated during the network optimization stage and so was retained as a descriptor in the final ANN model.

3.2 Use of ANN as a t_R predictor in environmental water samples

In wide-scope screening methods, where thousands of compounds are searched, it is of great importance to have secondary techniques for aid in the identification process. While reference standards can unequivocally confirm the identification of a compound, purchasing and maintaining standards for all compounds is prohibitively expensive. Furthermore, for many TPs, reference standards are not available and therefore alternate means for confidence in detection/identification are necessary. Although it is not comparatively informative as mass spectra, t_R prediction models can be very helpful in gaining more confidence in the obtained data and reducing time-consuming data processing. Prediction of t_R is best used at the beginning of this process and is especially useful when at a certain exact mass (i.e. (de)protonated molecule of a suspect compound), more than one chromatographic peak appears in the corresponding XIC.

Along these lines, and to test the “blind” skills of the ANN in a real environmental application, the 100 blind compounds as well as an additional set of compounds from our previous study not initially used into the ANN method (a total of 142 compounds), including primarily metabolites and TPs were searched. None of these compounds were in the training or verification sets used for ANN development. From this list of 142 compounds, 46 were finally selected and searched in 44 water samples (EWW, IWW and SW) using ChromaLynx and the ANN predicted t_R , based on their possible occurrence in the environment (**Table S2**) (Gracia-Lor et al., 2011, 2010; Hernández et al., 2015a; Zuccato et al., 2006). For further confidence, and to see how many false positive chromatographic peaks (above the intensity threshold) could be disregarded, fragment ions were also included in the detection process (**Table S3**). When a compound was identified on the basis of the accurate mass of the (de)protonated molecule and at least one fragment ion in at least one sample it was included in this test, leaving 26 compounds of various chemical classes and including nine metabolites, for only some of which standards were available in our laboratory (**Table 2**). The only compound found to have a t_R outside that of the ANN predicted 2 minute window was codeine. The incorporation of the ANN predicted t_R allowed almost half (49%) of all chromatographic peaks to be ignored, and even after removing codeine from the calculation, 48% could be disregarded. Furthermore, all but three compounds had a reduction in the median number of potential positive peaks, while 11 compounds had a

median value of only one chromatographic peak remaining after the introduction of the ANN predicted window.

In this section, examples are shown in the identification of losartan (originally tentatively identified with t_R prediction before a reference standard was purchased) and the tentative identification of the metabolites 10,11-dihydroxy carbamazepine and O-desmethyl venlafaxine (no reference standard available).

3.2.1 Assignment with reference standards

Losartan is a pharmaceutical used to treat hypertension that has been both predicted (Howard and Muir, 2013; Oosterhuis et al., 2013) and detected in environmental waters (Hernández et al., 2015a; Matsuo et al., 2011). Its presence in a suspect list is thus warranted, and its exact mass was incorporated into our HRMS database. When screening WW and SW samples, XICs at the exact mass of losartan (m/z 423.1700) resulted in two chromatographic peaks (4.63 and 10.13 minutes) (**Figure 2**, bottom left). The ANN t_R predictor was used and calculated a t_R of 9.95 minutes. This is almost exactly the t_R of one of the peaks, but it is worth noting that even after incorporating a ± 2 minute window only one peak warranted further investigation. Nevertheless, both peaks could have conceivably corresponded to losartan, therefore further research was conducted.

The LE and HE mass spectrum of the peak at 10.13 minutes was investigated for fragment ions: m/z 207.0917 ($C_{14}H_{11}N_2$, -2.4ppm), 377.1552 ($C_{22}H_{22}N_4Cl$, +5ppm) and 405.1590 ($C_{22}H_{22}N_4Cl$, -2.3ppm) (**Figure 2**, right). Literature (Hernández et al., 2015a) and the mass spectral database MassBank (Horai et al., 2010) were also searched to aid in the confidence of these fragment ions. It was found that these three fragment ions did indeed correspond to losartan. As seen in the figure, all associated fragments corresponded to the peak at 10.13 minutes, following the assertion of the t_R predictor. Furthermore, it is clearly seen that none of the fragment ions correspond with that of the other peak in the LE (4.63 minutes). A standard was later purchased and injected, unequivocally confirming that the peak at 10.13 minutes did correspond to losartan.

3.2.2 Tentative identification of metabolites without standard reference materials

The elimination of false positives in suspect analysis is challenging, especially the environmental matrices investigated herein (SW and WW) as thousands of compounds may be present. Suspect screening, by definition, does not rely on reference standards (Krauss et al., 2010). While the exact mass capability of HRMS has gone some way to avoid false positives, even at narrow mass window chromatograms, matrix inferences can be present, thereby hindering confident identification (Bade et al., 2015; Croley et al., 2012). A precise t_R predictor can therefore be a great additional means of identification.

Most research of emerging contaminants in the environment has focused on parent compounds, however many compounds can be at least partially metabolized or degraded in natural conditions (Jakimska et al., 2014). In this respect, the tentative identification of two major metabolites of carbamazepine and venlafaxine were explored: 10,11-dihydroxy carbamazepine and O-desmethyl venlafaxine (**Figure 3a**). More than one chromatographic peak was observed at the exact mass of each protonated molecule. The ANN t_R predictor was then used to try to help minimize the number of peaks to be analysed, with the predicted t_R calculated to be 6.29 and 5.76 minutes for 10,11-dihydroxy carbamazepine and O-desmethyl venlafaxine, respectively.

Two large (~4.00 and 6.66 minutes) and one small (~4.90 minutes) peaks are seen in the LE XIC of 10,11-dihydroxy carbamazepine ($m/z = 271.1080$). The predicted t_R was calculated to be 6.29 minutes and by including a ± 2 minute window as in Section 3.3.1, the large peak at ~4.00 minutes could be disregarded, leaving the peaks at 6.66 and ~4.90 minutes. The ability to focus on fewer peaks is the primary aim and benefit of t_R prediction in environmental screening applications for unknowns. While having only one (correct) peak remaining is ideal, being able to disregard some peaks gives credence to the use of t_R prediction in the identification process. To aid in the differentiation of these peaks, fragment ions were sought in literature, whereby one group performed an MS/MS experiment with a QTOF instrument to find the fragment ions of 10,11-dihydroxy carbamazepine (271.1080, 236.0706, 210.0913 and 180.0808) (Ferrer and Thurman, 2012). As the XICs in the figure show, all fragment ions have the peak at 6.65 minutes in common. This provides great confidence that this peak is indeed from 10,11-dihydroxy carbamazepine, however for unequivocal identification, a standard would still have to be purchased.

The example of O-desmethyl venlafaxine represented the worst case scenario, where no peaks could be removed after application of the ± 2 minute limit window. However, it must be noted that this was a rare case and only occurred for three of 26 compounds. In the LE XIC, two large (4.69 and 5.00 minutes) and two small peaks (~4.20 and 6.50 minutes) are seen. Even after incorporating the ANN predicted t_R and associated window (5.76 ± 2 minutes), all four peaks are still of interest. With the peaks being so close together, even using a ± 1.3 minute window (corresponding to ~80% of compounds being successfully inside this window) would result in the correct elimination of only one small peak. In this situation, fragment ions have to be used to

gain further information on the identity. Fragment ions were thus searched in literature (Herrera-Lopez et al., 2014) and investigated in the HE. **Figure 3b** shows all ions corresponding to the peak at 4.69 min. While the ANN predicted t_R and associated window did include O-desmethyl venlafaxine, all other peaks in the LE XIC were also inside, meaning that no further confidence could be gained by t_R prediction, rather through the investigation of fragment ions. Nevertheless, the combination of ANN predicted t_R and fragment ions led to the tentative identification of this compound.

While the examples explained here show the successful assignment of chromatographic peaks, it is impossible to have total confidence with t_R prediction. In cases where there is more than one peak in the XIC, and the predicted peak is found to be incorrect, the peaks slightly outside the prediction window will also have to be investigated. Nevertheless, with data processing nowadays being the most time consuming part of environmental screening methods, the time saved by incorporating t_R prediction outweighs the possibility of false negatives (and positives).

These examples clearly show the utility of ANN as a t_R predictor, not just for its ability to disregard some false positive peaks, but also for its accuracy and subsequent confidence for tentatively identified compounds. It is therefore recommended when performing large scope (e.g. >1000 compounds) screening of environmental samples to include accurate t_R prediction in the strategy used for identification. This is particularly useful in the investigation of metabolites and TPs, for which standards can be very costly or unavailable.

Conclusions

This work showed the development and use of a t_R predictor based on artificial neural networks. In particular, a four layer multilayer perceptron successfully modeled retention of 544 compounds under these separation conditions. Overall, 90 % of all compounds eluted within 2.00 minutes of the predicted value and for 100 blind test compounds, 95% were predicted within this window. The network was applied to additional suspect compound occurrence in wide-scope screening based on the use of LC-HRMS, demonstrating that it can reduce the number of false negatives or positives. This saves time and effort in the tentative identification of the compounds detected, as only those chromatographic peaks that fit the predicted t_R need to be focused on. Several representative examples are given to illustrate the usefulness of the complementary use of precise t_R prediction in large suspect screening of emerging contaminants. It is recommended to include this prediction for the identification of suspect compounds, particularly in the investigation of metabolites and TPs of organic contaminants, for which reference standards are commonly less accessible.

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Table 1: Summary of predicted t_R errors for all ANN test sets. Numbers given in italics are those which fall below the proposed 2-min window limit

Percentile of compounds	50	55	60	65	70	75	80	85	90	95
Predicted t_R error/min										
All sets (n=544)	<i>0.66</i>	<i>0.75</i>	<i>0.85</i>	<i>0.97</i>	<i>1.05</i>	<i>1.19</i>	<i>1.39</i>	<i>1.56</i>	<i>1.96</i>	2.80
Training set (n=344)	<i>0.70</i>	<i>0.81</i>	<i>0.89</i>	<i>1.02</i>	<i>1.13</i>	<i>1.24</i>	<i>1.45</i>	<i>1.70</i>	2.21	2.87
Verification set (n=100)	<i>0.51</i>	<i>0.59</i>	<i>0.64</i>	<i>0.76</i>	<i>0.89</i>	<i>0.99</i>	<i>1.35</i>	<i>1.44</i>	<i>1.60</i>	2.43
Blind test set (n=100)	<i>0.70</i>	<i>0.78</i>	<i>0.84</i>	<i>0.89</i>	<i>1.01</i>	<i>1.08</i>	<i>1.16</i>	<i>1.34</i>	<i>1.63</i>	<i>1.99</i>

Table 2: All compounds used for testing ANN predicted t_R , together with the number of samples each compound was detected, average number of peaks in the XIC and the ± 2 minute window and the predicted and sample t_R

Compound	Detection rate out of 44 samples	Median peaks per XIC (range)	Median peaks inside ± 2 min t_R window (range)		Predicted t_R (min)	Sample t_R (min)	Inaccuracy in predicted t_R (min)
10,11-dihydroxy carbamazepine ^a	30	2 (1-4)	1 (1-3)		6.29	6.66	0.37
2-hydroxy-terbutylazine ^b	6	6 (4-8)	2 (1-3)		4.24	5.50	1.26
4-desmethoxy omeprazole ^a	33	1 (1-2)	1 (1-2)		8.15	6.29	-1.86
4-formylamino-antipyrine ^{b,c}	37	2 (1-8)	2 (1-4)		3.53	3.70	0.17
a-hydroxy metoprolol ^a	17	5 (2-10)	3 (2-4)		2.73	3.30	0.57
Benzoylcegonine ^b	40	3 (1-6)	2 (1-5)		4.11	4.65	0.54
Bezafibrate ^b	2	6 (4-7)	1 (1-1)		10.80	10.78	-0.02
Caffeine ^a	40	3 (1-6)	1 (1-3)		3.17	3.83	0.66
Carbamazepine ^b	40	3 (1-10)	3 (1-5)		7.73	8.82	1.09
Carboxy losartan ^a	35	2 (1-3)	1 (1-1)		10.75	10.44	-0.31
Codeine ^b	25	5 (1-7)	1 (0-3)		4.85	2.46	-2.39
Cotinine ^a	32	10 (4-14)	5 (3-7)		2.00	1.81	-0.19
Diazinon ^{b,c}	4	3 (2-5)	2 (1-2)		11.64	12.50	0.86
Diclofenac ^b	13	1 (1-2)	1 (1-1)		11.71	12.17	0.46
Gemfibrozil ^b	13	4 (3-7)	2 (1-4)		12.29	13.34	1.05
Lidocaine ^a	40	5 (1-11)	2 (1-4)		5.21	4.24	-0.97
Lincomycin ^{b,c}	14	4 (2-8)	2 (1-4)		4.28	3.73	-0.55
Losartan ^b	42	2 (1-4)	2 (1-3)		9.95	10.13	-0.18
Metoprolol ^a	24	3 (1-9)	1 (1-3)		4.07	5.44	1.37
Naproxen ^b	32	7 (4-11)	2 (1-4)		10.06	10.54	0.48
O-desmethylvenlafaxine ^a	29	3 (2-5)	3 (1-5)		5.76	4.68	-1.08
Paraxanthine ^a	39	7 (2-12)	3 (2-4)		2.03	2.97	0.94
Ranitidine ^a	23	4 (2-6)	1 (1-1)		3.03	2.10	-0.93
Terbutylazine ^{b,c}	4	1 (1-3)	1 (1-2)		9.60	10.78	1.18
Trimethoprim ^b	32	7 (2-10)	4 (1-6)		3.11	3.52	0.41
Valsartan ^b	39	2 (1-7)	1 (1-3)		10.90	11.24	0.34

^a: Standard not available in laboratory. Sample t_R was based on HRMS data and the incorporation of fragment ions

^b: Standard available in laboratory

^c: Compound in blind set of ANN

Figures for Captions

Figure 1: TOP: Correlation of measured and predicted t_R for all compounds. The worst outliers in each set are also shown: A=atenolol (training set, error of -6.21 minutes); B=levamisole (verification set, +5.19 minutes); C=metosulam (blind set, +3.56 minutes). BOTTOM: Residual errors for all compounds in each dataset. For training, verification and blind test sets, n=344, 100 and 100 compounds respectively.

Figure 2: LEFT: eXtracted Ion Chromatograms (XICs) of losartan in an EWW sample, together with ANN t_R prediction (9.95 min) and associated ± 2 minute window (dotted lines; centre dashed line is the ANN-predicted value). RIGHT: Mass spectra from LE (bottom) and HE (top), showing fragment ions (423.158, 377.156, 207.092).

Figure 3: Tentative identification of 10,11-dihydroxy carbamazepine (a) and O-desmethyl venlafaxine (b) in an IWW and EWW sample respectively, together with ANN prediction and ± 2 minute window.

Figure 1

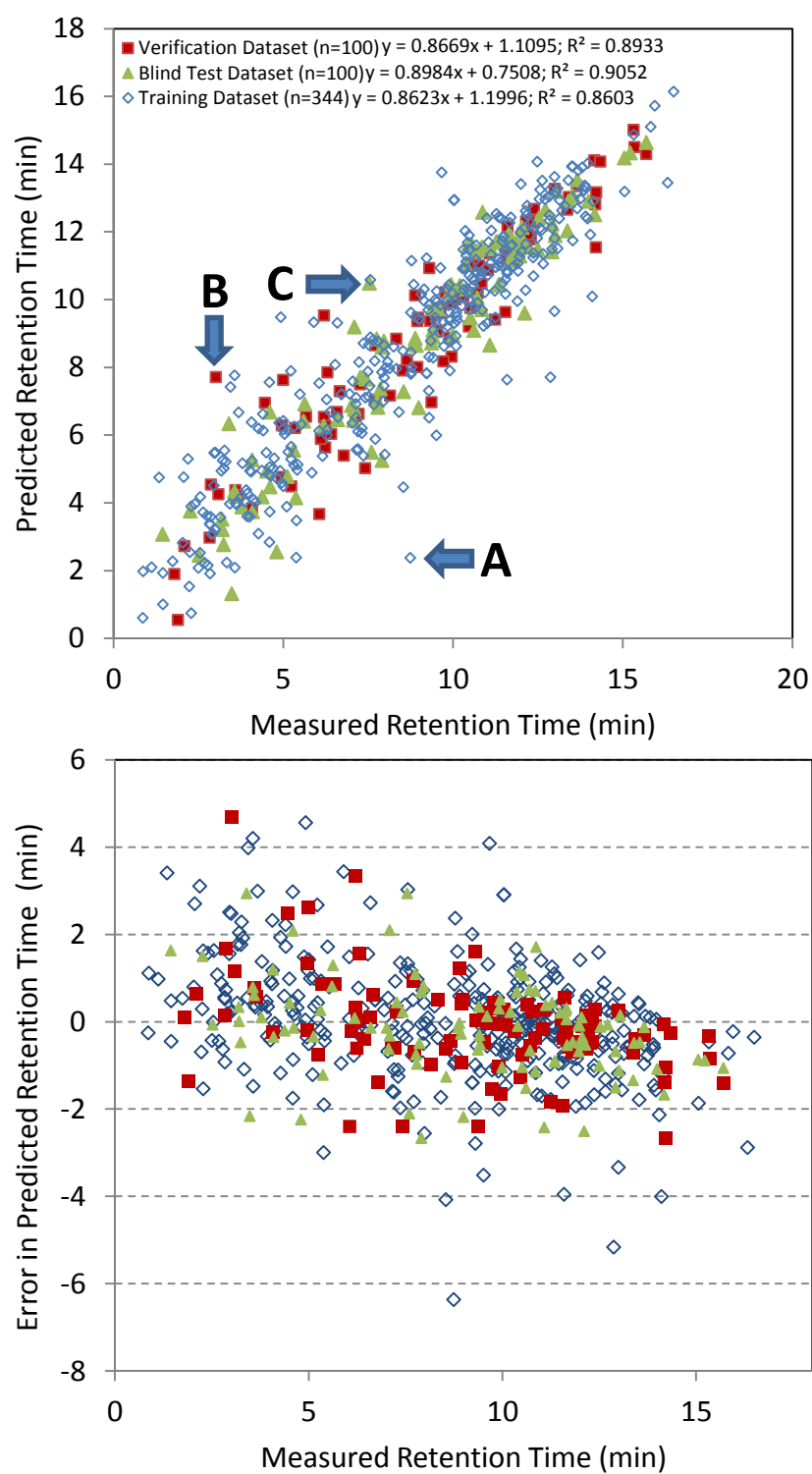


Figure 2:

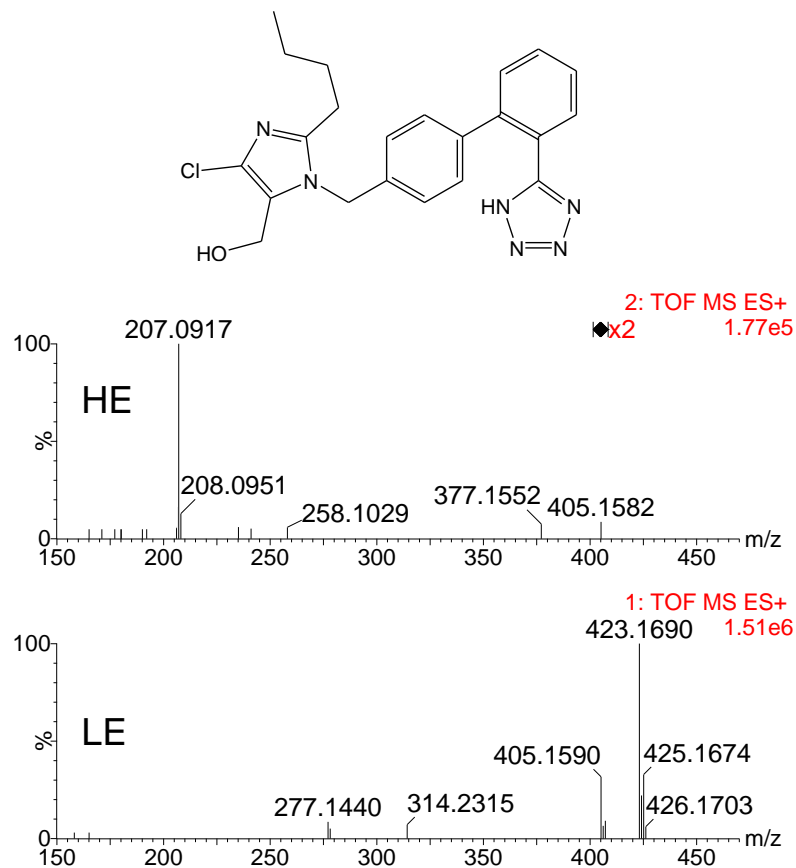
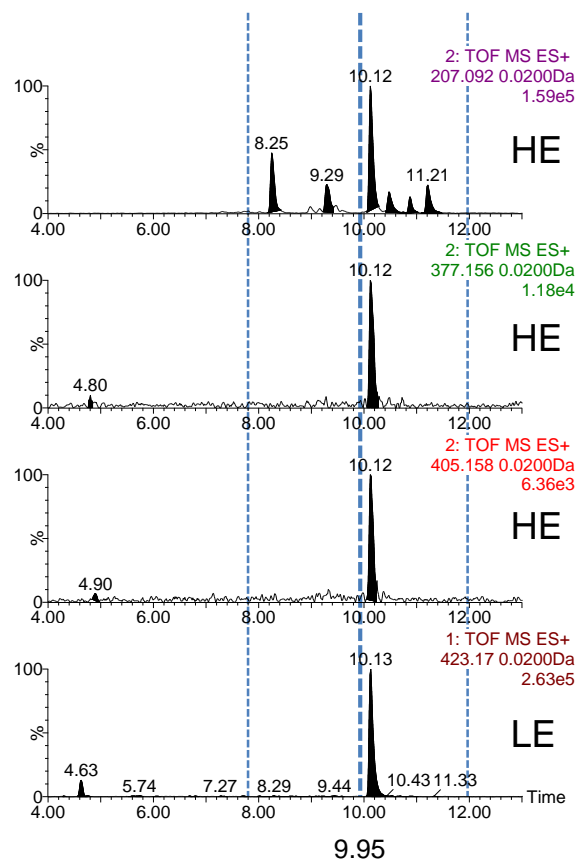


Figure 3:

